<u>RAW SEQUENCE LISTING</u>

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/539,954_

Source: _PY/10_

Date Processed by STIC: _6/30/05_

ENTERED

PCT

```
   3 <110> APPLICANT: Schmitz, Oliver
   4        Puzio, Piotr
   5        Blau, Astrid
   6        Looser, Ralf
   7        Wendel, Birgit
   8        Kamlage, Beate
   9        Plesch, Gunnar
  11 <120> TITLE OF INVENTION: Method for Producing Amino Acids
  13 <130> FILE REFERENCE: 13195-00006-US
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/539,954
C--> 15 <141> CURRENT FILING DATE: 2005-06-17
  15 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/014649
  16 <151> PRIOR FILING DATE: 2003-12-19
  18 <150> PRIOR APPLICATION NUMBER: DE 102 61 188.2
  19 <151> PRIOR FILING DATE: 2002-12-20
  21 <160> NUMBER OF SEQ ID NOS: 26
  23 <170> SOFTWARE: PatentIn version 3.3
  26 <210> SEQ ID NO: 1
  27 <211> LENGTH: 1164
  28 <212> TYPE: DNA
  29 <213> ORGANISM: Saccharomyces cerevisiae
  31 <220> FEATURE:
  32 <221> NAME/KEY: CDS
  33 <222> LOCATION: (1)..(1164)
  34 <223> OTHER INFORMATION: Threonine aldolase
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  38 Met Thr Glu Phe Glu Leu Pro Pro Lys Tyr Ile Thr Ala Ala Asn Asp
  39 1               5                   10                  15
  41 ttg cgg tca gac aca ttc acc act cca act gca gag atg atg gag gcc      96
  42 Leu Arg Ser Asp Thr Phe Thr Thr Pro Thr Ala Glu Met Met Glu Ala
  43             20                  25                  30
  45 gct tta gag gcc tct atc ggt gac gct gtc tac ggt gaa gat gtt gac     144
  46 Ala Leu Glu Ala Ser Ile Gly Asp Ala Val Tyr Gly Glu Asp Val Asp
  47         35                  40                  45
  49 acc gtt agg ctc gaa cag acc gtt gcc cgc atg gct ggc aaa gaa gca     192
  50 Thr Val Arg Leu Glu Gln Thr Val Ala Arg Met Ala Gly Lys Glu Ala
  51     50                  55                  60
  53 ggt ttg ttc tgt gtc tct ggg act ttg tcc aac cag att gcc atc aga     240
  54 Gly Leu Phe Cys Val Ser Gly Thr Leu Ser Asn Gln Ile Ala Ile Arg
  55 65                  70                  75                  80
  57 act cac ttg atg caa cct cca tac tct att cta tgt gat tac agg gct     288
  58 Thr His Leu Met Gln Pro Pro Tyr Ser Ile Leu Cys Asp Tyr Arg Ala
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59                     85                    90                    95
61 cac gtt tac act cac gaa gcc gct gga ctg gcg atc ttg tct caa gcg        336
62 His Val Tyr Thr His Glu Ala Ala Gly Leu Ala Ile Leu Ser Gln Ala
63                    100                   105                   110
65 atg gtg gtt cct gtg gtt cct tcc aac ggt gac tac ttg acc ttg gaa        384
66 Met Val Val Pro Val Val Pro Ser Asn Gly Asp Tyr Leu Thr Leu Glu
67           115                   120                   125
69 gac atc aag tca cac tac gtc cca gac gac ggt gat att cac ggt gcc        432
70 Asp Ile Lys Ser His Tyr Val Pro Asp Asp Gly Asp Ile His Gly Ala
71      130                   135                   140
73 ccc acc aga ttg att tct ctg gaa aac act tta cac ggt att gtt tat        480
74 Pro Thr Arg Leu Ile Ser Leu Glu Asn Thr Leu His Gly Ile Val Tyr
75 145                   150                   155                   160
77 cca ttg gaa gaa ctg gtc cgc atc aaa gct tgg tgt atg gaa aat ggt        528
78 Pro Leu Glu Glu Leu Val Arg Ile Lys Ala Trp Cys Met Glu Asn Gly
79                    165                   170                   175
81 ctc aaa cta cat tgt gac ggt gcc aga atc tgg aat gcc gct gca caa        576
82 Leu Lys Leu His Cys Asp Gly Ala Arg Ile Trp Asn Ala Ala Ala Gln
83                    180                   185                   190
85 tct ggc gtg cca tta aag caa tat ggg gaa atc ttc gac tcc atc tcc        624
86 Ser Gly Val Pro Leu Lys Gln Tyr Gly Glu Ile Phe Asp Ser Ile Ser
87           195                   200                   205
89 atc tgt cta tcc aag tct atg ggt gct cct att ggg tcc gtc ttg gtt        672
90 Ile Cys Leu Ser Lys Ser Met Gly Ala Pro Ile Gly Ser Val Leu Val
91      210                   215                   220
93 ggg aac ctt aag ttt gtc aag aag gcc acc cat ttc aga aaa caa caa        720
94 Gly Asn Leu Lys Phe Val Lys Lys Ala Thr His Phe Arg Lys Gln Gln
95 225                   230                   235                   240
97 ggt ggt ggt att aga caa tct ggt atg atg gct aga atg gct ctt gta        768
98 Gly Gly Gly Ile Arg Gln Ser Gly Met Met Ala Arg Met Ala Leu Val
99                    245                   250                   255
101 aac atc aac aac gat tgg aag tcc caa ttg ctg tac tcg cac tct ttg       816
102 Asn Ile Asn Asn Asp Trp Lys Ser Gln Leu Leu Tyr Ser His Ser Leu
103                    260                   265                   270
105 gct cat gaa tta gcc gaa tat tgt gag gca aag ggc atc ccg cta gag      864
106 Ala His Glu Leu Ala Glu Tyr Cys Glu Ala Lys Gly Ile Pro Leu Glu
107           275                   280                   285
109 tct cca gca gac acc aac ttt gtc ttt att aac ctg aag gcc gct aga       912
110 Ser Pro Ala Asp Thr Asn Phe Val Phe Ile Asn Leu Lys Ala Ala Arg
111      290                   295                   300
113 atg gac cca gat gtc ctt gtt aag aag ggt ttg aag tac aac gtt aag      960
114 Met Asp Pro Asp Val Leu Val Lys Lys Gly Leu Lys Tyr Asn Val Lys
115 305                   310                   315                   320
117 cta atg ggt ggt aga gtc tcg ttc cac tat caa gtc acc aga gat act      1008
118 Leu Met Gly Gly Arg Val Ser Phe His Tyr Gln Val Thr Arg Asp Thr
119                    325                   330                   335
121 ttg gaa aaa gtc aaa ttg gcc atc tcc gag gcc ttc gac tat gct aaa      1056
122 Leu Glu Lys Val Lys Leu Ala Ile Ser Glu Ala Phe Asp Tyr Ala Lys
123                    340                   345                   350
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125 gaa cat cct ttc gac tgt aac gga cct acc cag att tac cgt agt gaa    1104
126 Glu His Pro Phe Asp Cys Asn Gly Pro Thr Gln Ile Tyr Arg Ser Glu
127         355                 360                 365
129 tcc acc gag gtc gac gtt gat ggc aac gct atc cgc gaa ata aaa acc    1152
130 Ser Thr Glu Val Asp Val Asp Gly Asn Ala Ile Arg Glu Ile Lys Thr
131         370                 375                 380
133 tac aaa tac tga                                                    1164
134 Tyr Lys Tyr
135 385
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 387
140 <212> TYPE: PRT
141 <213> ORGANISM: Saccharomyces cerevisiae
143 <400> SEQUENCE: 2
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147 Leu Arg Ser Asp Thr Phe Thr Thr Pro Thr Ala Glu Met Met Glu Ala
148         20                  25                  30
150 Ala Leu Glu Ala Ser Ile Gly Asp Ala Val Tyr Gly Glu Asp Val Asp
151         35                  40                  45
153 Thr Val Arg Leu Glu Gln Thr Val Ala Arg Met Ala Gly Lys Glu Ala
154         50                  55                  60
156 Gly Leu Phe Cys Val Ser Gly Thr Leu Ser Asn Gln Ile Ala Ile Arg
157 65                  70                  75                  80
159 Thr His Leu Met Gln Pro Pro Tyr Ser Ile Leu Cys Asp Tyr Arg Ala
160             85                  90                  95
162 His Val Tyr Thr His Glu Ala Ala Gly Leu Ala Ile Leu Ser Gln Ala
163             100                 105                 110
165 Met Val Val Pro Val Val Pro Ser Asn Gly Asp Tyr Leu Thr Leu Glu
166             115                 120                 125
168 Asp Ile Lys Ser His Tyr Val Pro Asp Asp Gly Asp Ile His Gly Ala
169         130                 135                 140
171 Pro Thr Arg Leu Ile Ser Leu Glu Asn Thr Leu His Gly Ile Val Tyr
172 145                 150                 155                 160
174 Pro Leu Glu Glu Leu Val Arg Ile Lys Ala Trp Cys Met Glu Asn Gly
175             165                 170                 175
177 Leu Lys Leu His Cys Asp Gly Ala Arg Ile Trp Asn Ala Ala Ala Gln
178             180                 185                 190
180 Ser Gly Val Pro Leu Lys Gln Tyr Gly Glu Ile Phe Asp Ser Ile Ser
181             195                 200                 205
183 Ile Cys Leu Ser Lys Ser Met Gly Ala Pro Ile Gly Ser Val Leu Val
184         210                 215                 220
186 Gly Asn Leu Lys Phe Val Lys Lys Ala Thr His Phe Arg Lys Gln Gln
187 225                 230                 235                 240
189 Gly Gly Gly Ile Arg Gln Ser Gly Met Met Ala Arg Met Ala Leu Val
190             245                 250                 255
192 Asn Ile Asn Asn Asp Trp Lys Ser Gln Leu Leu Tyr Ser His Ser Leu
193             260                 265                 270
195 Ala His Glu Leu Ala Glu Tyr Cys Glu Ala Lys Gly Ile Pro Leu Glu
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196           275                   280                   285
198 Ser Pro Ala Asp Thr Asn Phe Val Phe Ile Asn Leu Lys Ala Ala Arg
199       290                   295                   300
201 Met Asp Pro Asp Val Leu Val Lys Lys Gly Leu Lys Tyr Asn Val Lys
202 305                   310                   315                   320
204 Leu Met Gly Gly Arg Val Ser Phe His Tyr Gln Val Thr Arg Asp Thr
205                   325                   330                   335
207 Leu Glu Lys Val Lys Leu Ala Ile Ser Glu Ala Phe Asp Tyr Ala Lys
208                   340                   345                   350
210 Glu His Pro Phe Asp Cys Asn Gly Pro Thr Gln Ile Tyr Arg Ser Glu
211       355                   360                   365
213 Ser Thr Glu Val Asp Val Asp Gly Asn Ala Ile Arg Glu Ile Lys Thr
214       370                   375                   380
216 Tyr Lys Tyr
217 385
220 <210> SEQ ID NO: 3
221 <211> LENGTH: 376
222 <212> TYPE: PRT
223 <213> ORGANISM: Canola
225 <400> SEQUENCE: 3
226 Gly Cys Phe Ala Cys Tyr Leu Val Gly Gly Phe Ser Val Gln Glu Lys
227 1             5                   10                  15
229 Met Val Thr Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro
230             20                  25                  30
232 Thr Glu Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp
233             35                  40                  45
235 Val Leu Gly Tyr Asp Pro Thr Ala Phe Arg Leu Glu Thr Glu Met Ala
236       50                  55                  60
239 Lys Thr Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met
240 65                  70                  75                  80
242 Gly Asn Leu Val Ser Val Leu Val His Cys Asp Val Arg Gly Ser Glu
243             85                  90                  95
245 Val Ile Leu Gly Asp Asn Cys His Ile Asn Ile Phe Glu Asn Gly Gly
246             100                 105                 110
248 Ile Ala Thr Ile Gly Gly Val His Pro Arg Gln Val Lys Asn Asn Asp
249       115                 120                 125
251 Asp Gly Thr Met Asp Ile Asp Leu Ile Glu Ala Ala Ile Arg Asp Pro
252       130                 135                 140
254 Met Gly Glu Leu Phe Tyr Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn
255 145                 150                 155                 160
257 Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp
258             165                 170                 175
260 Arg Val Gly Glu Leu Ala Lys Lys His Gly Leu Lys Leu His Ile Asp
261             180                 185                 190
263 Gly Ala Arg Ile Phe Asn Ala Ser Val Ala Leu Gly Val Pro Val Asp
264       195                 200                 205
266 Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly
267 210                 215                 220
269 Ile Gly Ala Pro Val Gly Ser Val Ile Val Gly Ser Lys Asn Phe Ile
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270 225                   230                 235                 240
272 Ala Lys Ala Arg Arg Leu Arg Lys Thr Leu Gly Gly Gly Met Arg Gln
273             245                 250                 255
275 Ile Gly Leu Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Val
276             260                 265                 270
278 Gly Lys Leu Glu Ser Asp His Lys Lys Ala Arg Leu Leu Ala Asp Gly
279         275                 280                 285
281 Leu Asn Glu Val Lys Gly Leu Arg Val Asp Ala Cys Ser Val Glu Thr
282     290                 295                 300
284 Asn Met Val Phe Ile Asp Ile Glu Glu Gly Thr Lys Thr Arg Ala Glu
285 305                 310                 315                 320
287 Lys Ile Cys Lys Tyr Met Glu Glu Arg Gly Ile Leu Val Met Gln Glu
288             325                 330                 335
290 Ser Ser Ser Arg Met Arg Val Val Leu His His Gln Ile Ser Ala Ser
291             340                 345                 350
293 Asp Val Gln Tyr Ala Leu Ser Cys Phe Gln Gln Ala Leu Ala Val Lys
294         355                 360                 365
296 Gly Val Gln Lys Glu Met Gly Asn
297     370                 375
300 <210> SEQ ID NO: 4
301 <211> LENGTH: 115
302 <212> TYPE: PRT
303 <213> ORGANISM: Soybean
305 <400> SEQUENCE: 4
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309 Pro Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro Ser Glu
310             20                  25                  30
312 Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Val Leu
313         35                  40                  45
315 Gly Arg Asp Pro Ser Cys Phe Arg Leu Glu Thr Glu Met Ala Lys Ile
316     50                  55                  60
318 Leu Gly Lys Glu Gly Ala Leu Phe Val Pro Ser Gly Thr Met Ala Asn
319 65                  70                  75                  80
321 Leu Ile Ser Val Leu Val His Cys Asp Ile Arg Gly Ser Glu Val Ile
322             85                  90                  95
324 Leu Gly Asp Asn Ser His Ile His Ile Tyr Glu Asn Gly Gly Ile Ala
325             100                 105                 110
327 Thr Leu Gly
328         115
331 <210> SEQ ID NO: 5
332 <211> LENGTH: 127
333 <212> TYPE: PRT
334 <213> ORGANISM: Rice
336 <220> FEATURE:
337 <221> NAME/KEY: misc_feature
338 <222> LOCATION: (1)..(127)
339 <223> OTHER INFORMATION: unknown or other
341 <220> FEATURE:
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/30/2005
PATENT APPLICATION: US/10/539,954   TIME: 09:07:42

Input Set : **A:\Final sequence list-13195-00006-US.txt**
Output Set: **N:\CRF4\06302005\J539954.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 4
Seq#:7; Xaa Pos. 5

VERIFICATION SUMMARY   DATE: 06/30/2005
PATENT APPLICATION: **US/10/539,954**   TIME: 09:07:42

Input Set : **A:\Final sequence list-13195-00006-US.txt**
Output Set: **N:\CRF4\06302005\J539954.raw**

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
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